

IN THE CLAIMS:

Applicant, pursuant to 37 C.F.R. § 1.121, submits the following amendments to the claims:

1. (Currently amended) A method for detecting methylated nucleic acids comprising:
contacting a nucleic acid sample suspected of containing methylated nucleotides with an oligonucleotide probe under suitable conditions for nucleic acid hybridization, said oligonucleotide probe comprising a first stem labeled with a fluorophore moiety, a loop sequence having a region of nucleotides complementary to at least a region of the nucleic acid that is susceptible to methylation, and a second stem labeled with a quencher moiety that is capable of quenching the fluorophore moiety when in ~~sufficient~~ spatial proximity to the fluorophore moiety, and wherein the nucleotides forming the first stem are capable of moving into spatial proximity with the nucleotides forming the second stem when the probe is dissociated from the nucleic acid sample;
altering the hybridization conditions such that the oligonucleotide probe dissociates from unmethylated nucleic acids but remains hybridized to methylated nucleic acids; and
measuring the change in fluorescence,
wherein an increase in fluorescence indicates methylated nucleotides in said nucleic acid sample.
2. (Previously presented) The method of claim 1, wherein upon probe dissociation from the target nucleic acid the first and second stem hybridize together causing quenching of the fluorophore moiety.
3. (Previously presented) The method of claim 1, wherein the loop sequence contains at least 10 nucleotides.
4. (Previously presented) The method of claim 1, wherein the loop sequence contains at least 35 nucleotides.
5. (Previously presented) The method of claim 1, wherein the loop sequence contains at least 25 nucleotides.

6. (Previously presented) The method of claim 1, wherein the loop sequence contains from about 15 to about 20 nucleotides.

7. (Previously presented) The method of claim 1, wherein when the loop sequence is complementary to a portion of a nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

8. (Previously presented) The method of claim 1, wherein when the loop sequence is complementary to a portion of a Myf-3 nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

9. (Currently amended) The method of claim 8, wherein nucleic acid sequence that undergoes methylation is ~~the loop sequence is complementary to at least one of the sequences selected from the group consisting of SEQ ID NOS:1-3 and methylated CpG-containing variants thereof.~~

10. (Previously presented) The method of claim 1, wherein when the loop sequence is complementary to a portion of a glutathione-S-transferase-II (pi) nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

11. (Currently amended) The method of claim 10, wherein the nucleic acid sequence that undergoes methylation is ~~loop sequence is complementary to at least one of the sequences selected from the group consisting of SEQ ID NOS:4-5 and methylated CpG-containing variants thereof.~~

12. (Previously presented) The method of claim 1, wherein when the loop sequence is complementary to a portion of a calcitonin nucleic acid sequence that undergoes methylation when a cell transforms from a normal state to a cancerous state.

13. (Previously presented) The method of claim 1, wherein the method is used to detect abnormally methylated gene sequences in prostate cancer tissues.

14. (Previously presented) The method of claim 1, wherein altering the hybridization conditions comprises altering the temperature of the hybridization reaction.

15. (Previously presented) The method of claim 1, wherein the stem sequences do not

hybridise to the target gene and are of a sufficiently short length to avoid non-specific binding between the stem and any other nucleic acid sequence in the reaction mixture.

16. (Previously presented) The method of claim 1, wherein the stem sequences are at least 4 to 8 nucleotides in length.

17. (Previously presented) The method of claim 1, wherein at least one of the stem sequences contains a methylated cytosine residue.

18. (Cancelled).